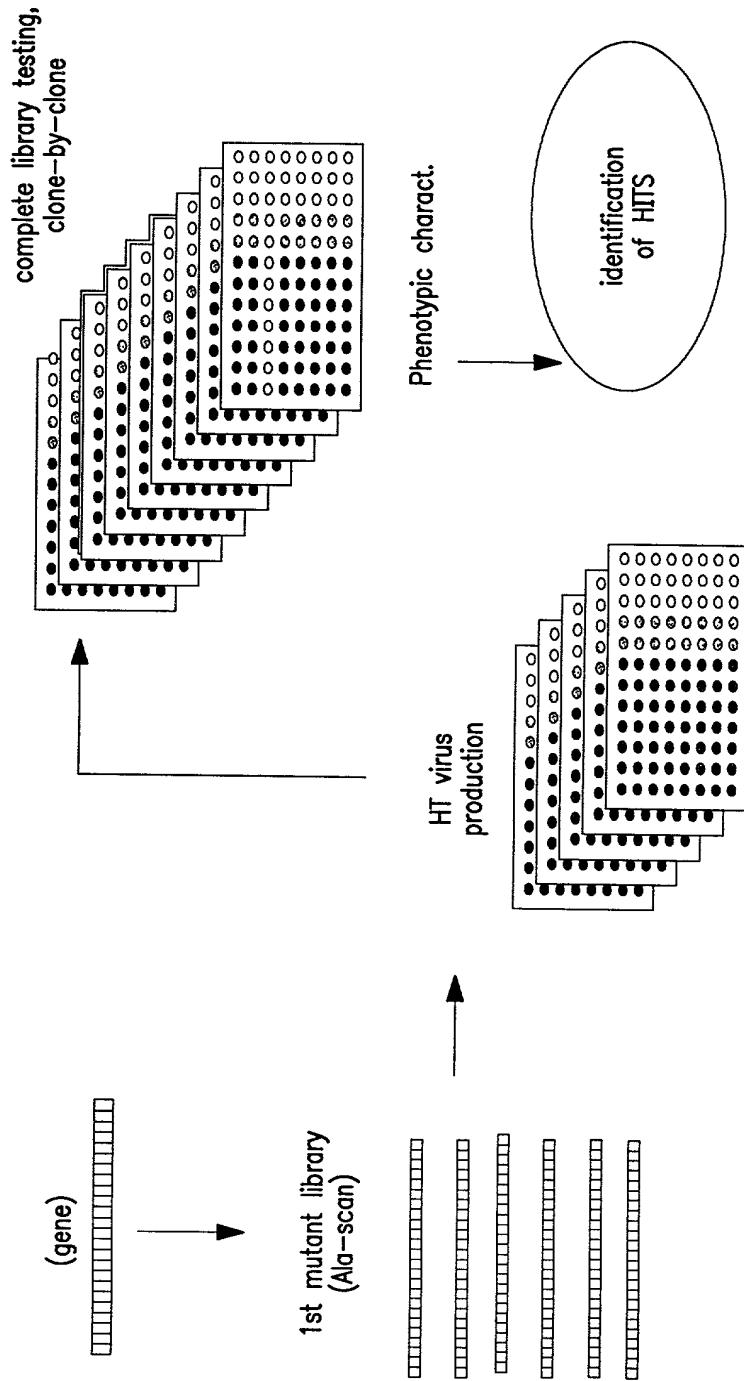
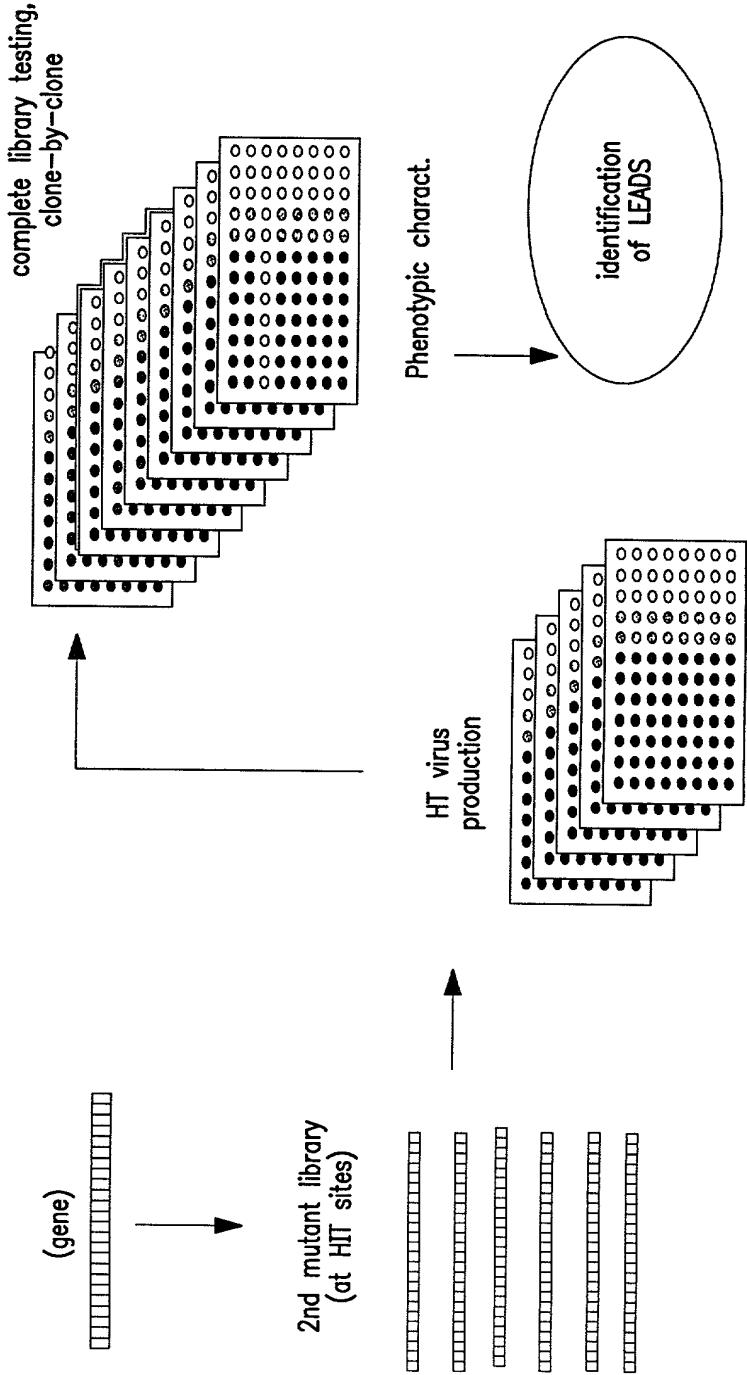


***1st Round: screening of mutants (full length  $\Delta\alpha$ -scan)***



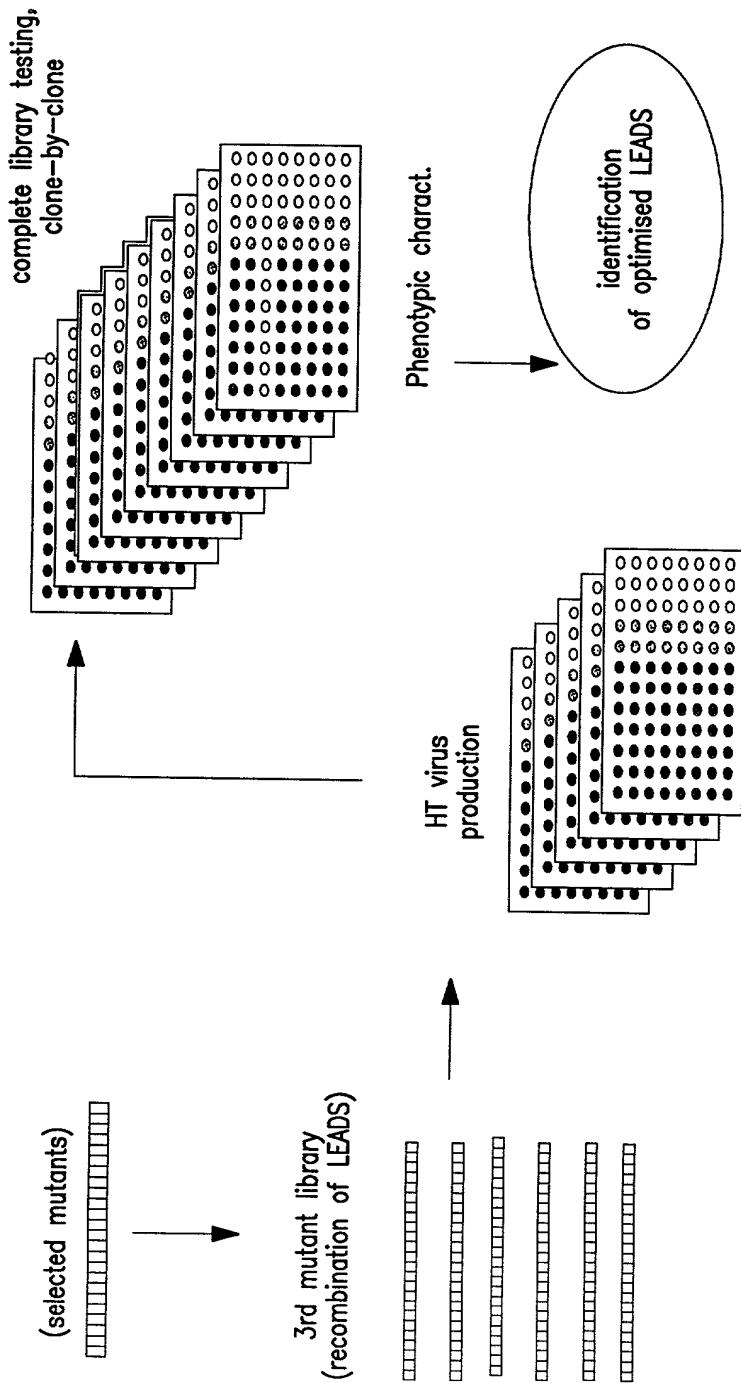
**FIG. 1A**

***2nd Round: screening of mutants at (surrounding) HTT positions***



**FIG. 1B**

**3rd Round: screening of recombinants between LEADS**



**FIG. IC**

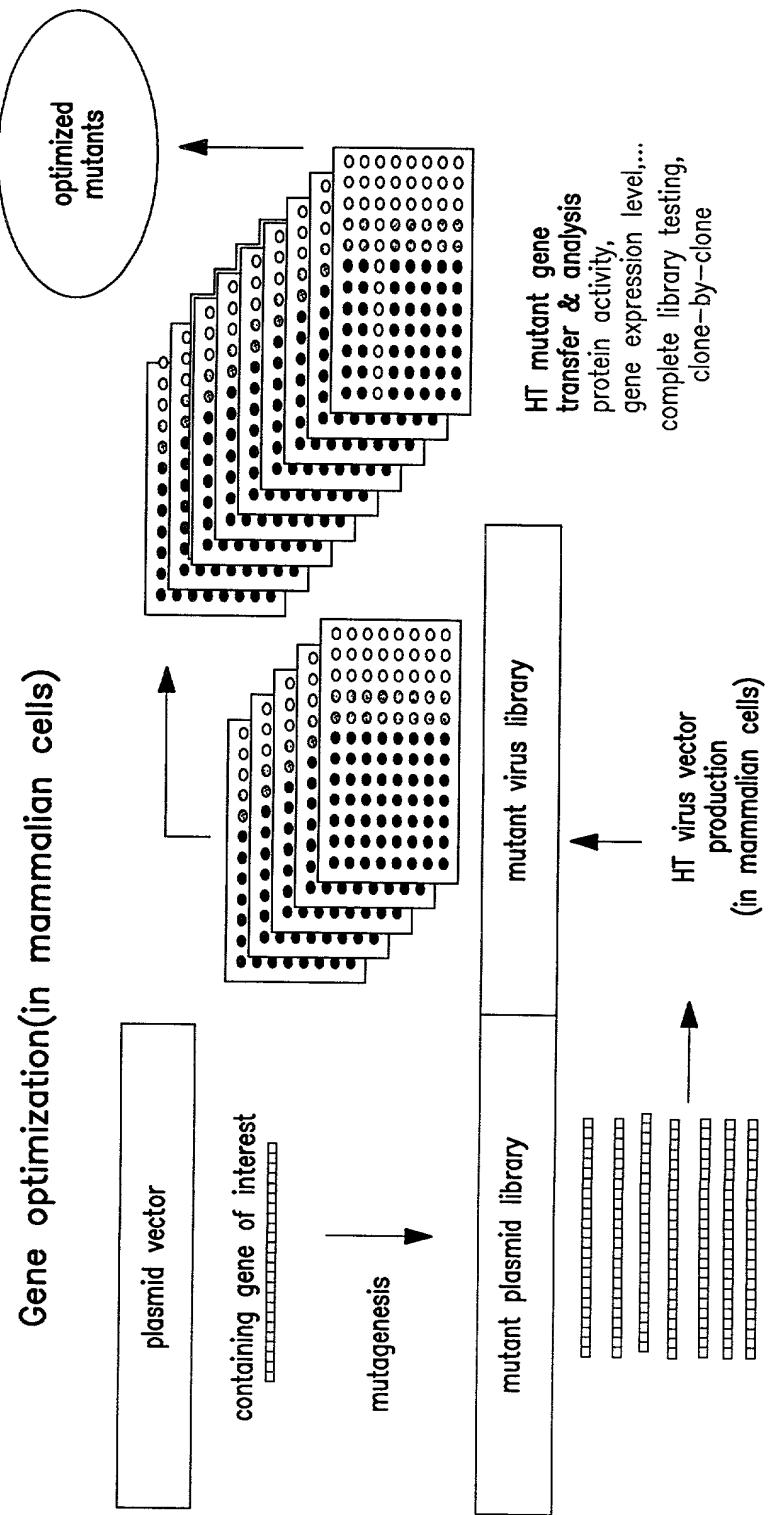


FIG. D

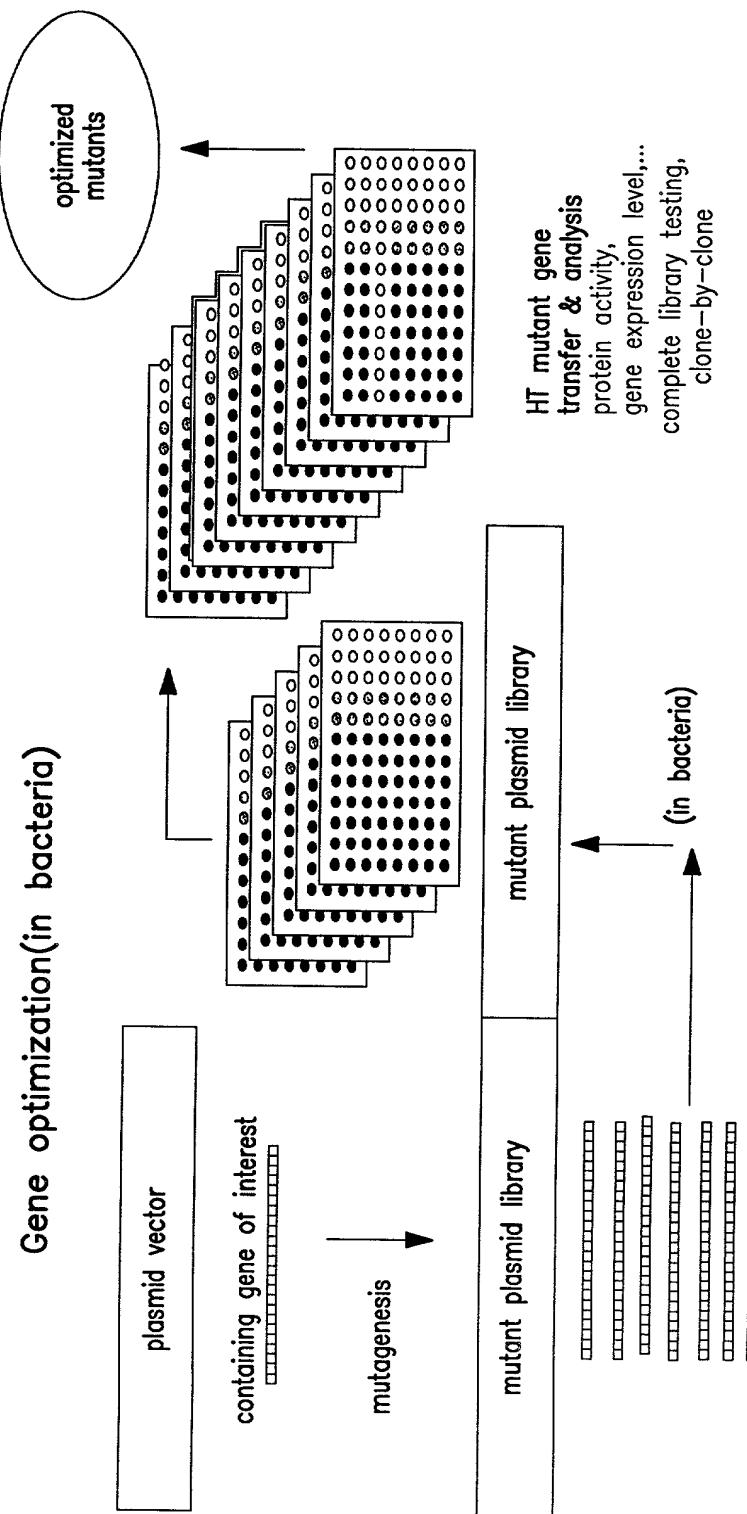


FIG. E

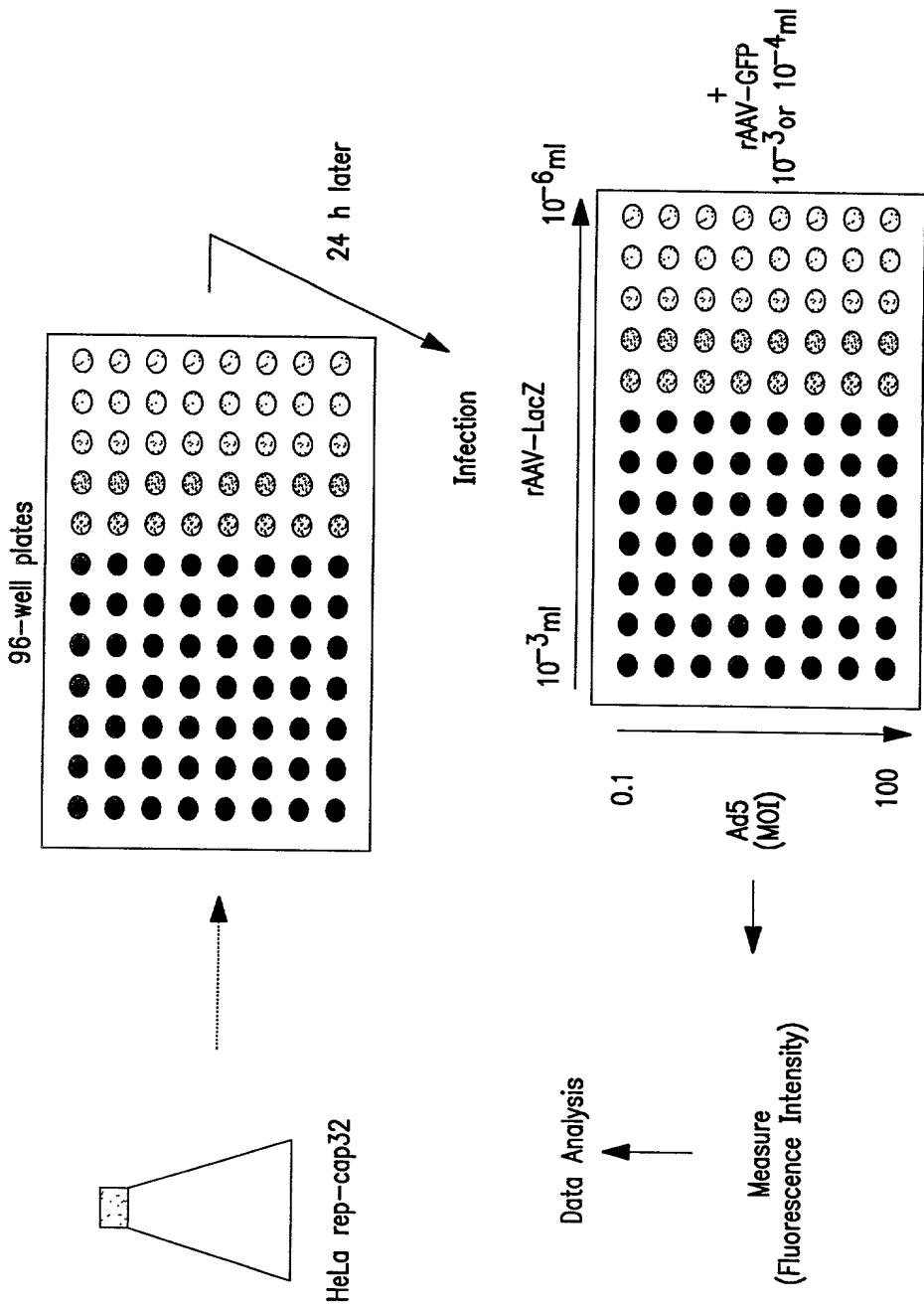


FIG. 2A

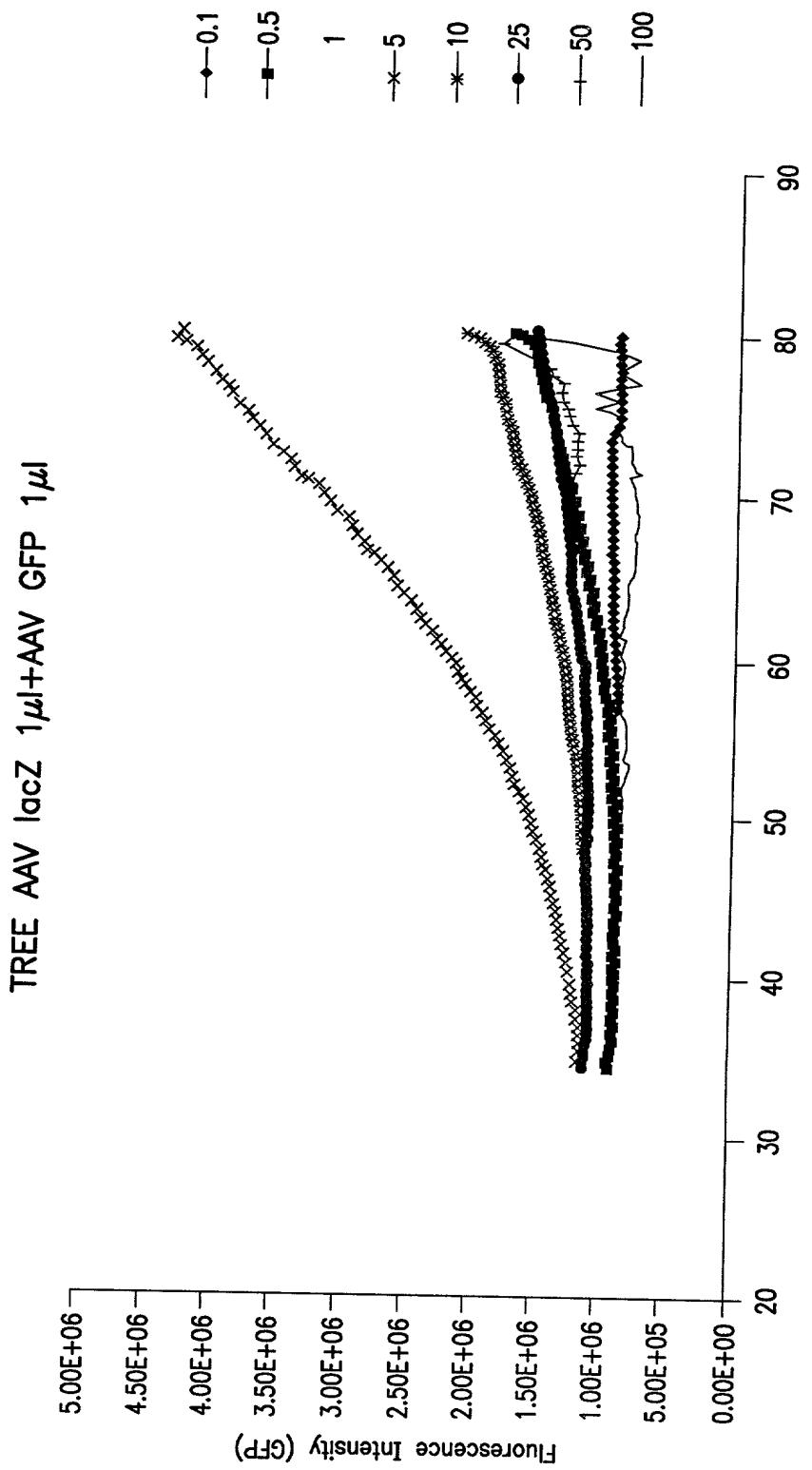


FIG. 2B

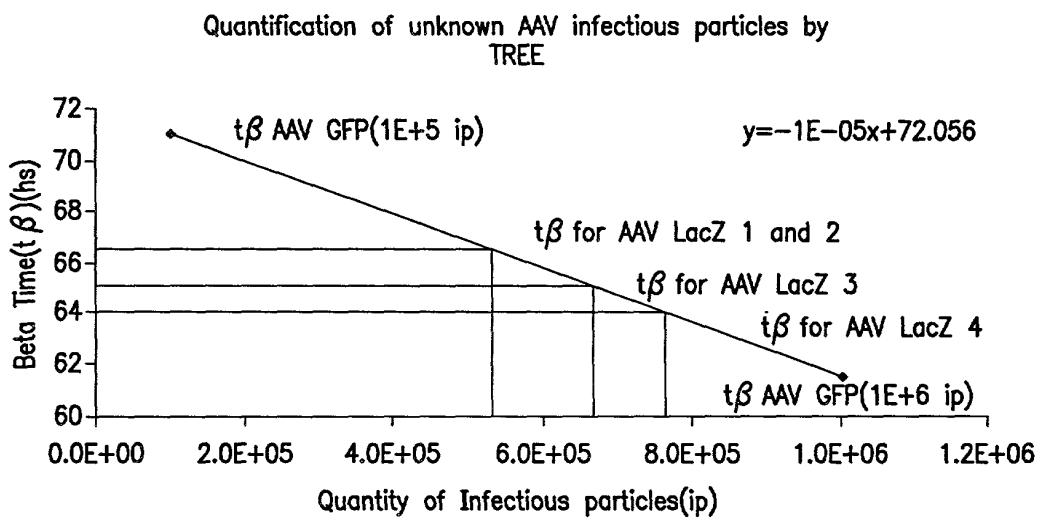
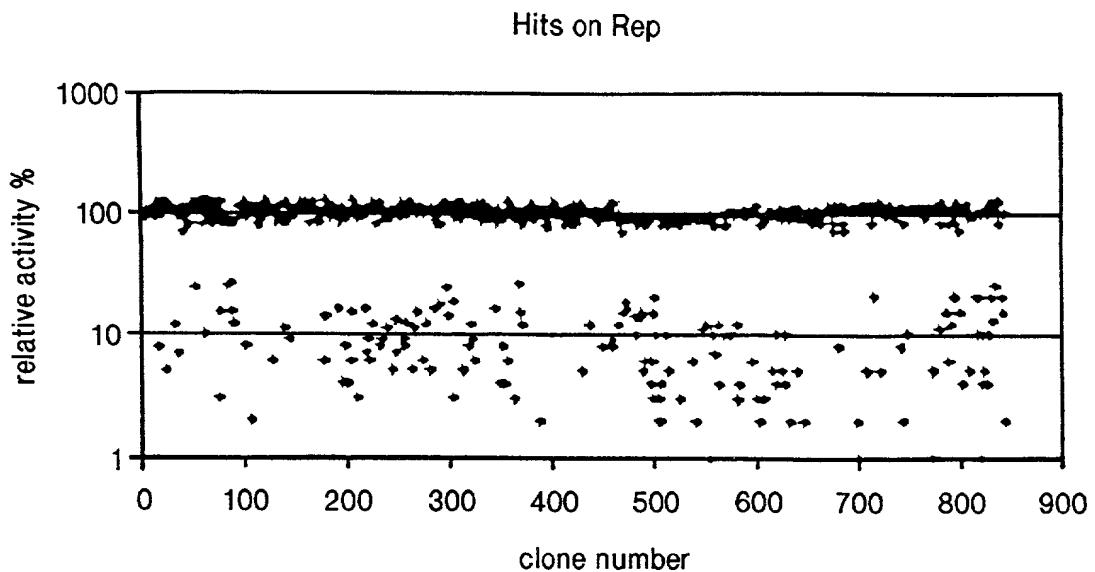
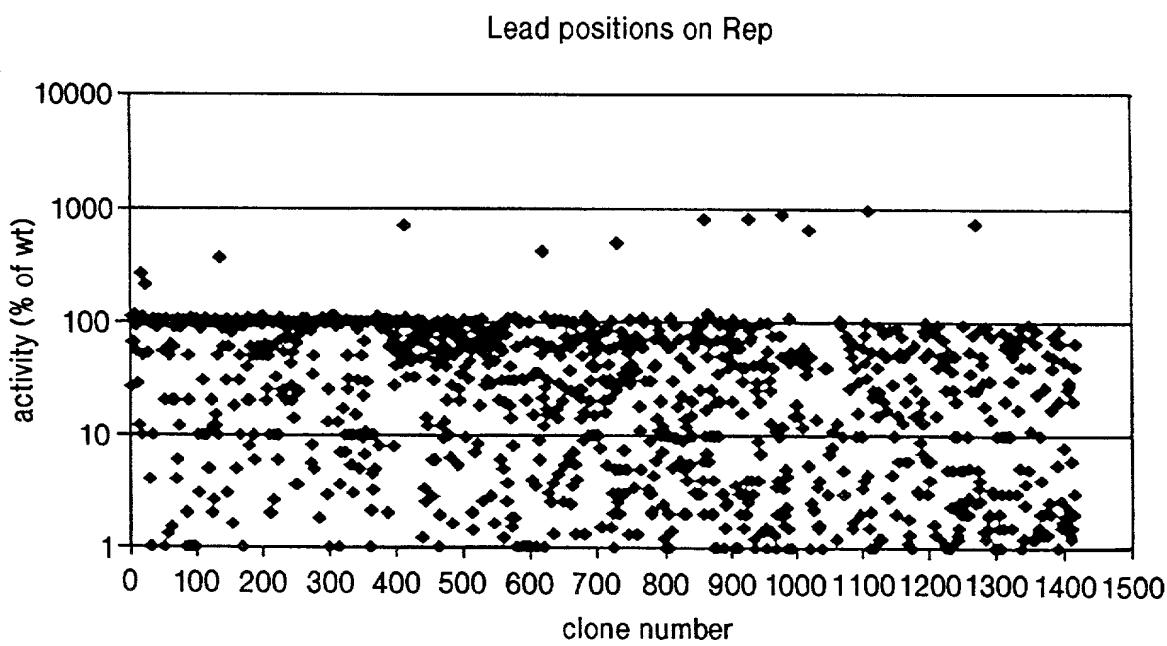


FIG. 2C



**FIG. 3A**



**FIG. 3B**

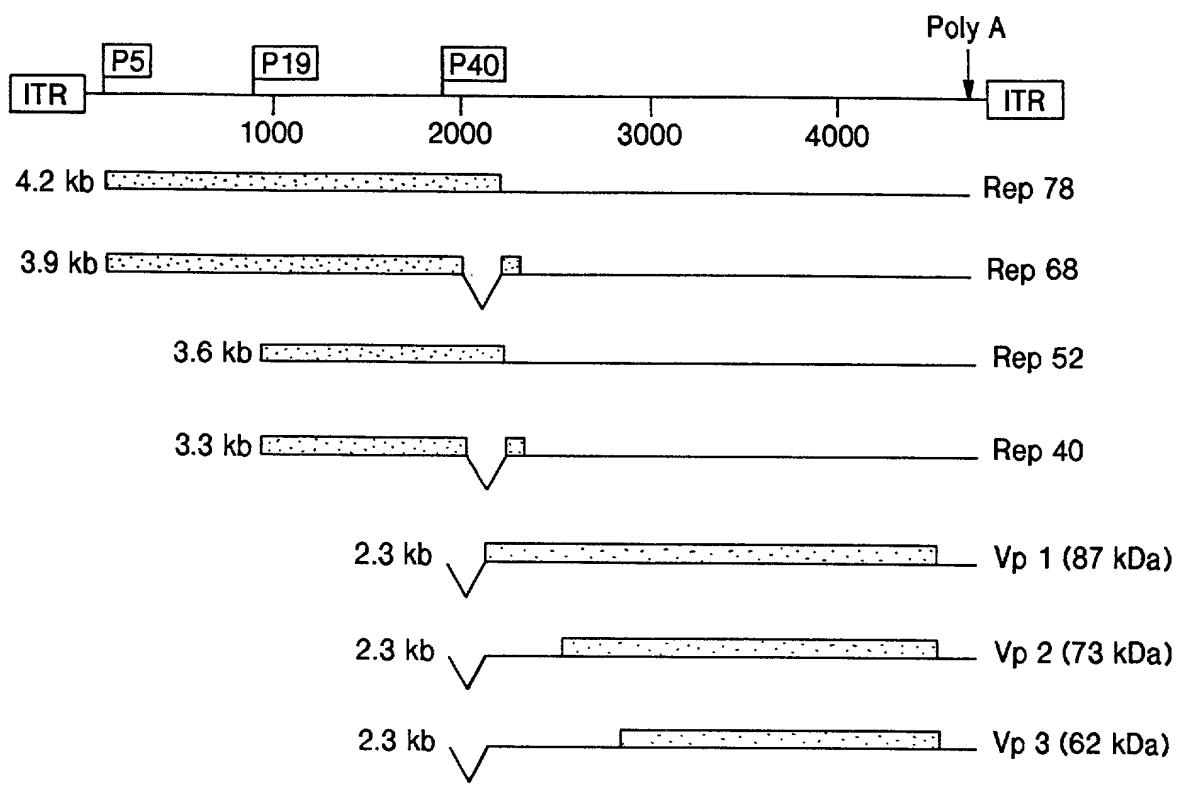


FIG. 4

	10	20	30	40	50	60	
1	MPGFYEIVIKVPSDLDEHLPGISDSFVSWAEKEWELPPSDMDILNLIEQAPLTVAEKLQ						60
2	MPGFYEIVIKVPSDLDEHLPGISDSFVNVAEKEWELPPSDMDILNLIEQAPLTVAEKLQ						60
3	MPGFYEIVLKVPSDLDEHLPGISNSFVNVAEKEWELPPSDMDPNLIEQAPLTVAEKLQ						60
4	MPGFYEIVLKVPSDLDEHLPGISNSFVNVAEKEWELPPSDMDPNLIEQAPLTVAEKLQ						60
5	MPGFYEIVLKVPSDLDEHLPGISDSFVSWAEKEWELPPSDMDILNLIEQAPLTVAEKLQ						60
6	MPGFYEIVIKVPSDLGHLPGISDSFVNVAEKEWELPPSDMDILNLIEQAPLTVAEKLQ						60
7	MATFYEVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTVEQPQLTVADRIR						60
C	M***FYE***:V*P*D***HLPGIS+SFV:WV****WELPP*SD***+*L*EQ**LTVA****						
	70	80	90	100	110	120	
1	RDFLVQWRRVSKAPEALFFFQFEKGESYFHLHILVETTGVKSMVILGRFLSQIRDKLVQTI						120
2	RDFLVQWRRVSKAPEALFFFQFEKGESYFHLHILVETTGVKSMVILGRFLSQIRDKLVQTI						120
3	REFLVEWRRVSKAPEALFFFQFEKGETYFHLHVLIELTIGVKSMVVGRYVSQIKEKLVTRI						120
4	REFLVEWRRVSKAPEALFFFQFEKGETYFHLHVLIELTIGVKSMVVGRYVSQIKEKLVTRI						120
5	REFLVEWRRVSKAPEALFFFQFEKGETYFHLHVLIELTIGVKSMVVGRYVSQIKEKLVTRI						120
6	RDFLTEWRRVSKAPEALFFFQFEKGESYFHMVLVETTGVKSMVILGRFLSQIREKLIQRI						120
7	RVFLYEWNKFSKQ-ESKFFVQFEKGSEYFHLHTLVETSGISSLVMLGRYVSQIRAQLVKVV						119
C	R:FL++W***SK**E***FFVQFEKG+:YFH*H:L+ET:G**SMV:GR::SQI::*L::*						
	130	140	150	160	170	180	
1	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL						180
2	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL						180
3	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL						180
4	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL						180
5	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYISACL						180
6	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEQYLSACL						180
7	FQGIEPQINDWVAITKVKK--GGANKVVDSGYIPAYLLPKVQPELQWAWTNLDEYKLAAL						177
C	**G:EP:***W*A*TK*****GG*NKVVD: *YIP*YLLPK*QPELQWAWTN*:Y: *A*L						
	190	200	210	220	230	240	
1	NLAERKRLVAQHLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK						240
2	NLAERKRLVAHDLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK						240
3	NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK						240
4	NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK						240
5	NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK						240
6	NLTERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDKGITSEK						240
7	NLEERKRLVAQFLAESSQRS-QEAASQREFSADPVIKSSTSQKYMALVNWLVEHGISKEK						236
C	NL+ERKRLVA*+L***SQ***Q***+***S**PVI*SKTS**YM*LV*WL*+GITSEK						
	250	260	270	280	290	300	
1	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR						300
2	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR						300
3	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPEDITKNRIYQ						300
4	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPEDITKNRIYQ						300
5	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVQNPEDISSNRIYR						300
6	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVQQPVEDISSNRIYK						300
7	QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKRIWQ						296
C	QWIQE*Q*SY*SFN***NSRSQIKAALDNA:KIM+LTK:A*DYLVG: :**+DI: :NRI: :						
	310	320	330	340	350	360	
1	ILELNGYEPAYAGSVFLGWAQKRGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
2	ILELNGYDPAYAGSVFLGWAQKRGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
3	ILELNGYDPQYAASAVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
4	ILELNGYDPQYAASAVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
5	ILEMNGYDPQYAASAVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
6	ILELNGYDPQYAASAVFLGWATKKFGKRNTIWLFGPATTGKTNIAEAIJAHAVPFYGCVNWT						360
7	IFEMNGYDPAYAGSILYGCQRFSNKRNTVWLYGPATTGKTNIAEAIJAHAVPFYGCVNWT						356
C	I*E+NGY*P:YA:S***GW***:F*KRNT*WL*GPATTGKTNIAEAIJAH+VPFYGCVNWT						

FIG. 5A

	370	380	390	400	410	420
1	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS					
2	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS					
3	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIEPTPVIVTS					
4	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIEPTPVIVTS					
5	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS					
6	NENFPFNDVDKMKVIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS					
7	NENFPFNDVDKMKLIWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSVQIDSTPVIVTS					
C	NENFPFNDVDKMK*IWEEGKMT*KVVESAKAILGGSKVRVDQKCKSS*QI+*TPVIVTS					
	430	440	450	460	470	480
1	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHEHFGVTKQEVKEFFRWAQDHVTEV					
2	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHEHFGVTKQEVKEFFRWAQDHVTEV					
3	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHDHFGVTKQEVKDFFRWASDHVTDV					
4	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHDHFGVTKQEVKDFFRWASDHVTDV					
5	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHDHFGVTKQEVKDFFRWASDHVTEV					
6	NTNMCVIDGNSTTFEHQPLQDRMFKFELTRRLHDHFGVTKQEVKDFFRWAKDHVVEV					
C	NTNMCVVVDGNSTTFEHQPLQDRMFKFELTRRLHDHFGVTKQEVKDFFRWAKVNQPV					
	476					
	NTNMC*V*DGNSTTFEHQPL*DRMFKFELT+RL: *DFGK*TKQEVK+FF*WA: ***+: V					
	490	500				
1	AHEFYVRKGGAALKRPAAPDDADKSEPKRA-----				510	520
2	AHEFYVRKGGAALKRPAAPDDADKSEPKRA-----				CPSVADPSTSDAEG	522
3	AHEFYVRKGGAALKRPAASNDADVSEPKRQ-----				CPSVADPSTSDAEG	522
4	AHEFYVRKGGAALKRPAASNDADVSEPKRQ-----				CTSLAQPTTSDAEA	522
5	THEFYVRKGGAALKRPAAPNDADISEPKRA-----				CTSLAQPTTSDAEA	522
6	EHEFYVKKGGAALKRPAAPSDADISEPKRV-----				CPSVAQPSTSDAEA	522
7	THEFKVPRELAGTKGAEKSLKRPLGDVTNTSYKSLEKRARLSFVPETPRSSDVTVDPAPL				RESVAQPSTSDAEA	522
C	:HEF*V+****A:****A:****.*****: +:****:****A: :				536	
	530	540	550	560	570	580
1	APVDFADRYQNKCSRHAQMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESEQ					
2	APVDFADRYQNKCSRHAQMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESEQ					
3	P-ADYADRYQNKCSRHVGMNLMLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV					
4	P-ADYADRYQNKCSRHVGMNLMLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV					
5	P-VDYADRYQNKCSRHVGMNLMLFPCKTCERMNQNVDICFTHGVMDCAEFCFP--VSESEQPV					
6	S-INYADRYQNKCSRHVGMNLMLFPCKTCERMNQNSNICFTHGQKDCLECFP--VSESEQPV					
7	RPLNWNSRYDCKCDYHAQFDNISNKDCECEYLNRGKNGCICHNVTHCQICHG-----					
C	::::+****RY**KC**H:****:****C:CE**N*:****C**H:****C.*C**.::::+:::					
	588					
	590	600	610	620		
1	PVVRKRTYRKLCIAIHLLGRAPEIACSAACLVDNVLDLDDCVSEQ					623
2	PVVRKRTYRKLCIAIHLLGRAPEIACSAACLVDNVLDLDDCVSEQ					623
3	SVVKKKTYQKLCPIIHHILGRAPEIACSAACLVDNVLDLDDCVSEQ					624
4	SVVKKKTYQKLCPIIHHILGRAPEIACSAACLVDNVLDLDDCVSEQ					624
5	SVVRKRTYQKLCPIIHHIMGRAPEVACSAACLVDNVLDLDDCDMEQ					624
6	VSVVKKAYQKLCYIHHIMG-KVPDFACTACDLNVNVDLDDCIFEQ					623
7	-----IPPWEKENLSDFGDFDDANKEQ					621
C	:+*:****:****:****:****:****:****:****:****:****:EO					610

**FIG. 5B**